

STN

FIL MEDLINE BIOSIS EMBASE SCISEARCH CAPLUS USPATFULL PCTFULL

=> s sodium and channel and polymorphism and (hh1b or hh1?)

L1 61 SODIUM AND CHANNEL AND POLYMORPHISM AND (HH1B OR HH1?)

=> dup rem l1

PROCESSING COMPLETED FOR L1

L2 53 DUP REM L1 (8 DUPLICATES REMOVED)

=> s l1 and py<=2002

2 FILES SEARCHED...

4 FILES SEARCHED...

L3 32 L1 AND PY<=2002

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 5, 2004, 20:37:48 ; Search time 22471 Seconds
(without alignments)
11748.584 Million cell updates/sec

Title: US-10-077-054-1
Perfect score: 6091
Sequence: 1 gatgagaagatggcaaactt.....ggccaggacacactgaaaag 6091

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*

28: em_un:*
 29: em_vi:*
 30: em_htg_hum:*
 31: em_htg_inv:*
 32: em_htg_other:*
 33: em_htg_mus:*
 34: em_htg_pln:*
 35: em_htg_rod:*
 36: em_htg_mam:*
 37: em_htg_vrt:*
 38: em_sy:*
 39: em_htgo_hum:*
 40: em_htgo_mus:*
 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query					
No.	Score	Match	Length	DB	ID	Description	
1	6091	100.0	6091	9	AF482988	AF482988 Homo sapi	
2	6079.8	99.8	8414	9	AY038064	AY038064 Homo sapi	
3	6075.6	99.7	6169	9	AY148488	AY148488 Homo sapi	
4	6039.6	99.2	8491	6	AX449276	AX449276 Sequence	
5	6039.6	99.2	8491	6	AX741279	AX741279 Sequence	
6	6039.6	99.2	8491	9	HUMHH1A	M77235 Human cardi	
7	6038	99.1	8491	6	AX449278	AX449278 Sequence	
8	5993.6	98.4	6048	6	AR183727	AR183727 Sequence	
9	5990.4	98.3	6048	6	AR337848	AR337848 Sequence	
10	5385.4	88.4	8530	6	AX552195	AX552195 Sequence	
11	5119.6	84.1	6394	4	CFA555547	AJ555547 Canis fam	
12	5094	83.6	6503	4	BTA251721	AJ251721 Bos tauru	
13	5014.8	82.3	7545	10	RATSCAL	M27902 Rat cardiac	
14	5013.4	82.3	6458	10	MMU271477	AJ271477 Mus muscu	
15	4727.6	77.6	5901	6	AX348083	AX348083 Sequence	
16	4727.6	77.6	5901	10	AF353637	AF353637 Rattus no	
17	2553.6	41.9	6527	6	A58859	A58859 Sequence 7	
18	2553.6	41.9	6527	6	AR230064	AR230064 Sequence	
19	2550.8	41.9	6524	6	A58853	A58853 Sequence 1	
20	2550.8	41.9	6524	6	AR230061	AR230061 Sequence	
21	2550.8	41.9	6524	6	AX710158	AX710158 Sequence	
22	2550.8	41.9	6524	10	RNSNS	X92184 R.norvegicu	
23	2549.6	41.9	6344	6	AR253318	AR253318 Sequence	
24	2549.6	41.9	6344	6	AX252389	AX252389 Sequence	
25	2549.6	41.9	6344	10	RNU53833	U53833 Rattus norv	
26	2508.8	41.2	6726	4	CFU60590	U60590 Canis famil	
27	2487	40.8	5874	6	AR253325	AR253325 Sequence	
28	2485.4	40.8	5874	6	AX252393	AX252393 Sequence	
29	2485.4	40.8	5874	6	AX710162	AX710162 Sequence	
30	2485.4	40.8	5874	9	AF117907	AF117907 Homo sapi	
31	2432.8	39.9	6373	6	AX252391	AX252391 Sequence	
32	2432.8	39.9	6373	10	MMSNS	Y09108 M.musculus	
33	2243	36.8	6007	6	AR181336	AR181336 Sequence	

34	2243	36.8	6586	10	AF049240	AF049240 Rattus no
35	2225.4	36.5	6586	6	AR181360	AR181360 Sequence
36	2221.6	36.5	7052	6	A58857	A58857 Sequence 5
37	2221.6	36.5	7052	6	AR230063	AR230063 Sequence
38	2214.4	36.4	5977	6	AR181335	AR181335 Sequence
39	2214.4	36.4	6556	6	AR181338	AR181338 Sequence
40	2214.4	36.4	6556	10	AF049239	AF049239 Rattus no
41	2204.2	36.2	5937	10	AF049617	AF049617 Mus muscu
42	2167.4	35.6	6826	6	AR181339	AR181339 Sequence
43	2167.4	35.6	6826	10	RATSCP6A	L39018 Rattus norv
44	2098.6	34.5	7008	6	AX741281	AX741281 Sequence
45	2098.6	34.5	7008	9	AB027567	AB027567 Homo sapi